

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bryan, Bruce
 (ii) TITLE OF THE INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
 (iii) NUMBER OF SEQUENCES: 14
 (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Brown, Martin, Haller & McClain
 (B) STREET: 1660 Union Street
 (C) CITY: San Diego
 (D) STATE: CA
 (E) COUNTRY: USA
 (F) ZIP: 92101-2926
 (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ Version 1.5
 (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE: 11-25-96
 (C) CLASSIFICATION:
 (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 08/597,274
 (B) FILING DATE: 02-06-96
 (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Seidman, Stephanie L
 (B) REGISTRATION NUMBER: 33,779
 (C) REFERENCE/DOCKET NUMBER: 6680-105
 (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 619-238-0999
 (B) TELEFAX: 619-238-0062
 (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (ix) FEATURE:
 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...942
 (D) OTHER INFORMATION: Renilla Reinformis Luciferase
 (x) PUBLICATION INFORMATION:
 PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGC	TTA	AAG	ATG	ACT	TCG	AAA	GTT	TAT	GAT	CCA	GAA	CAA	AGG	AAA	CGG	48
Ser	Leu	Lys	Met	Thr	Ser	Lys	Val	Tyr	Asp	Pro	Glu	Gln	Arg	Lys	Arg	
1				5					10					15		
ATG	ATA	ACT	GGT	CCG	CAG	TGG	TGG	GCC	AGA	TGT	AAA	CAA	ATG	AAT	GTT	96
Met	Ile	Thr	Gly	Pro	Gln	Trp	Trp	Ala	Arg	Cys	Lys	Gln	Met	Asn	Val	
			20					25					30			
CTT	GAT	TCA	TTT	ATT	AAT	TAT	TAT	GAT	TCA	GAA	AAA	CAT	GCA	GAA	AAT	144
Leu	Asp	Ser	Phe	Ile	Asn	Tyr	Tyr	Asp	Ser	Glu	Lys	His	Ala	Glu	Asn	
		35				40						45				
GCT	GTT	ATT	TTT	TTA	CAT	GGT	AAC	GCG	GCC	TCT	TCT	TAT	TTA	TGG	CGA	192
Ala	Val	Ile	Phe	Leu	His	Gly	Asn	Ala	Ala	Ser	Ser	Tyr	Leu	Trp	Arg	
	50					55					60					
CAT	GTT	GTG	CCA	CAT	ATT	GAG	CCA	GTA	GCG	CGG	TGT	ATT	ATA	CCA	GAT	240
His	Val	Val	Pro	His	Ile	Glu	Pro	Val	Ala	Arg	Cys	Ile	Ile	Pro	Asp	
65					70					75					80	
CTT	ATT	GGT	ATG	GGC	AAA	TCA	GGC	AAA	TCT	GGT	AAT	GGT	TCT	TAT	AGG	288
Leu	Ile	Gly	Met	Gly	Lys	Ser	Gly	Lys	Ser	Gly	Asn	Gly	Ser	Tyr	Arg	
				85					90					95		
TTA	CTT	GAT	CAT	TAC	AAA	TAT	CTT	ACT	GCA	TGG	TTG	AAC	TTC	TTA	ATT	336
Leu	Leu	Asp	His	Tyr	Lys	Tyr	Leu	Thr	Ala	Trp	Leu	Asn	Phe	Leu	Ile	
			100					105					110			
TAC	CAA	AGA	AGA	TCA	TTT	TTT	GTC	GGC	CAT	GAT	TGG	GGT	GCT	TGT	TTG	384
Tyr	Gln	Arg	Arg	Ser	Phe	Phe	Val	Gly	His	Asp	Trp	Gly	Ala	Cys	Leu	
		115					120					125				
GCA	TTT	CAT	TAT	AGC	TAT	GAG	CAT	CAA	GAT	AAG	ATC	AAA	GCA	ATA	GTT	432
Ala	Phe	His	Tyr	Ser	Tyr	Glu	His	Gln	Asp	Lys	Ile	Lys	Ala	Ile	Val	
	130					135					140					
CAC	GCT	GAA	AGT	GTA	GTA	GAT	GTG	ATT	GAA	TCA	TGG	GAT	GAA	TGG	CCT	480
His	Ala	Glu	Ser	Val	Val	Asp	Val	Ile	Glu	Ser	Trp	Asp	Glu	Trp	Pro	
145					150					155					160	
GAT	ATT	GAA	GAA	GAT	ATT	GCG	TTG	ATC	AAA	TCT	GAA	GAA	GGA	GAA	AAA	528
Asp	Ile	Glu	Glu	Asp	Ile	Ala	Leu	Ile	Lys	Ser	Glu	Glu	Gly	Glu	Lys	
				165					170					175		
ATG	GTT	TTG	GAG	AAT	AAC	TTC	TTC	GTG	GAA	ACC	ATG	TTG	CCA	TCA	AAA	576
Met	Val	Leu	Glu	Asn	Asn	Phe	Phe	Val	Glu	Thr	Met	Leu	Pro	Ser	Lys	
			180					185					190			
ATC	ATG	AGA	AAG	TTA	GAA	CCA	GAA	GAA	TTT	GCA	GCA	TAT	CTT	GAA	CCA	624
Ile	Met	Arg	Lys	Leu	Glu	Pro	Glu	Phe	Ala	Ala	Tyr	Leu	Glu	Pro		
		195					200					205				
TTC	AAA	GAG	AAA	GGT	GAA	GTT	CGT	CGT	CCA	ACA	TTA	TCA	TGG	CCT	CGT	672
Phe	Lys	Glu	Lys	Gly	Glu	Val	Arg	Arg	Pro	Thr	Leu	Ser	Trp	Pro	Arg	
	210					215					220					
GAA	ATC	CCG	TTA	GTA	AAA	GGT	GGT	AAA	CCT	GAC	GTT	GTA	CAA	ATT	GTT	720
Glu	Ile	Pro	Leu	Val	Lys	Gly	Gly	Lys	Pro	Asp	Val	Val	Gln	Ile	Val	
225					230					235					240	
AGG	AAT	TAT	AAT	GCT	TAT	CTA	CGT	GCA	AGT	GAT	GAT	TTA	CCA	AAA	ATG	768
Arg	Asn	Tyr	Asn	Ala	Tyr	Leu	Arg	Ala	Ser	Asp	Asp	Leu	Pro	Lys	Met	
				245					250					255		

TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC	816
Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly	
260 265 270	
GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT	864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His	
275 280 285	
TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG	912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser	
290 295 300	
TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA TTACTTTGGT TTTTATTTA	965
Phe Val Glu Arg Val Leu Lys Asn Glu Gln	
305 310	
CATTTTTCCTT GGGTTTAATA ATATAAATGT CATTTTCAAC AATTTTATTT TAACTGAATA	1025
TTTCACAGGG AACATTCATA TATGTTGATT AATTTAGCTC GAACTTTACT CTGTCATATC	1085
ATTTTGGAAT ATTACCTCTT TCAATGAAAC TTTATAAACA GTGGTTCAAT TAATTAATAT	1145
ATATTATAAT TACATTTGTT ATGTAATAAA CTCGGTTTAA TTATAAAAAA A	1196

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1821 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1665
- (D) OTHER INFORMATION: Cypridina hilgendorffii luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: EP 0 387 355 TORAY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG AAG CTA ATA ATT CTG TCT ATT ATA TTG GCC TAC TGT GTC ACA GTC	48
Met Lys Leu Ile Ile Leu Ser Ile Ile Leu Ala Tyr Cys Val Thr Val	
1 5 10 15	
AAC TGC CAG GAT GCA TGT CCT GTA GAA GCT GAA GCA CCG TCA AGT ACA	96
Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr	
20 25 30	
CCA ACA GTC CCA ACA TCT TGT GAA GCT AAA GAA GGA GAA TGT ATC GAT	144
Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp	
35 40 45	
ACC AGA TGC GCA ACA TGT AAA CGA GAC ATA CTA TCA GAC GGA CTG TGT	192
Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys	
50 55 60	
GAA AAT AAA CCA GGG AAG ACA TGC TGT AGA ATG TGC CAG TAT GTA ATT	240
Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile	
65 70 75 80	
GAA TCC AGA GTA GAA GCT GCT GGA TAT TTT AGA ACG TTT TAC GCC AAA	288
Glu Ser Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Ala Lys	
85 90 95	

AGA	TTT	AAT	TTT	CAG	GAA	CCT	GGT	AAA	TAT	GTG	CTG	GCT	CGA	GGA	ACC	336
Arg	Phe	Asn	Phe	Gln	Glu	Pro	Gly	Lys	Tyr	Val	Leu	Ala	Arg	Gly	Thr	
			100					105					110			
AAG	GGT	GGC	GAC	TGG	TCT	GTA	ACC	CTC	ACC	ATG	GAG	AAT	CTA	GAT	GGA	384
Lys	Gly	Gly	Asp	Trp	Ser	Val	Thr	Leu	Thr	Met	Glu	Asn	Leu	Asp	Gly	
		115					120					125				
CAG	AAG	GGA	GCT	GTA	CTG	ACT	AAG	ACA	ACA	CTG	GAG	GTA	GTA	GGA	GAC	432
Gln	Lys	Gly	Ala	Val	Leu	Thr	Lys	Thr	Thr	Leu	Glu	Val	Val	Gly	Asp	
	130					135					140					
GTA	ATA	GAC	ATT	ACT	CAA	GCT	ACT	GCA	GAT	CCT	ATC	ACA	GTT	AAC	GGA	480
Val	Ile	Asp	Ile	Thr	Gln	Ala	Thr	Ala	Asp	Pro	Ile	Thr	Val	Asn	Gly	
145					150					155					160	
GGA	GCT	GAC	CCA	GTT	ATC	GCT	AAC	CCG	TTC	ACA	ATT	GGT	GAG	GTG	ACC	528
Gly	Ala	Asp	Pro	Val	Ile	Ala	Asn	Pro	Phe	Thr	Ile	Gly	Glu	Val	Thr	
				165					170					175		
ATT	GCT	GTT	GTC	GAA	ATA	CCC	GGC	TTC	AAT	ATT	ACA	GTC	ATC	GAA	TTC	576
Ile	Ala	Val	Val	Glu	Ile	Pro	Gly	Phe	Asn	Ile	Thr	Val	Ile	Glu	Phe	
			180					185					190			
TTT	AAA	CTA	ATC	GTG	ATA	GAT	ATT	CTG	GGA	GGA	AGA	TCT	GTG	AGA	ATT	624
Phe	Lys	Leu	Ile	Val	Ile	Asp	Ile	Leu	Gly	Gly	Arg	Ser	Val	Arg	Ile	
		195				200					205					
GCT	CCA	GAC	ACA	GCA	AAC	AAA	GGA	CTG	ATA	TCT	GGT	ATC	TGT	GGT	AAT	672
Ala	Pro	Asp	Thr	Ala	Asn	Lys	Gly	Leu	Ile	Ser	Gly	Ile	Cys	Gly	Asn	
	210					215					220					
CTG	GAG	ATG	AAT	GAC	GCT	GAT	GAC	TTT	ACT	ACA	GAC	GCA	GAT	CAG	CTG	720
Leu	Glu	Met	Asn	Asp	Ala	Asp	Asp	Phe	Thr	Thr	Asp	Ala	Asp	Gln	Leu	
225					230					235				240		
GCG	ATC	CAA	CCC	AAC	ATA	AAC	AAA	GAG	TTC	GAC	GGC	TGC	CCA	TTC	TAC	768
Ala	Ile	Gln	Pro	Asn	Ile	Asn	Lys	Glu	Phe	Asp	Gly	Cys	Pro	Phe	Tyr	
				245				250						255		
GGG	AAT	CCT	TCT	GAT	ATC	GAA	TAC	TGC	AAA	GGT	CTC	ATG	GAG	CCA	TAC	816
Gly	Asn	Pro	Ser	Asp	Ile	Glu	Tyr	Cys	Lys	Gly	Leu	Met	Glu	Pro	Tyr	
			260					265					270			
AGA	GCT	GTA	TGT	CGT	AAC	AAT	ATC	AAC	TTC	TAC	TAT	TAC	ACT	CTG	TCC	864
Arg	Ala	Val	Cys	Arg	Asn	Asn	Ile	Asn	Phe	Tyr	Tyr	Tyr	Thr	Leu	Ser	
		275					280					285				
TGC	GCC	TTC	GCT	TAC	TGT	ATG	GGA	GGA	GAA	GAA	AGA	GCT	AAA	CAC	GTC	912
Cys	Ala	Phe	Ala	Tyr	Cys	Met	Gly	Gly	Glu	Glu	Arg	Ala	Lys	His	Val	
	290					295					300					
CTT	TTC	GAC	TAT	GTT	GAG	ACA	TGC	GCT	GCA	CCG	GAA	ACG	AGA	GGA	ACG	960
Leu	Phe	Asp	Tyr	Val	Glu	Thr	Cys	Ala	Ala	Pro	Glu	Thr	Arg	Gly	Thr	
305					310					315					320	
TGT	GTT	TTA	TCA	GGA	CAT	ACT	TTC	TAT	GAC	ACA	TTC	GAC	AAA	GCC	AGA	1008
Cys	Val	Leu	Ser	Gly	His	Thr	Phe	Tyr	Asp	Thr	Phe	Asp	Lys	Ala	Arg	
				325					330					335		
TAT	CAA	TTC	CAG	GGC	CCA	TGC	AAA	GAG	CTT	CTG	ATG	GCC	GCA	GAC	TGT	1056
Tyr	Gln	Phe	Gln	Gly	Pro	Cys	Lys	Glu	Leu	Leu	Met	Ala	Ala	Asp	Cys	
			340					345					350			
TAC	TGG	AAC	ACA	TGG	GAT	GTA	AAG	GTT	TCA	CAT	AGA	GAT	GTT	GAG	TCA	1104

Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser
 355 360 365
 TAC ACT GAG GTA GAG AAA GTA ACA ATC AGG AAA CAG TCA ACT GTA GTA 1152
 Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val
 370 375 380
 GAT TTG ATT GTG GAT GGC AAG CAG GTC AAG GTT GGA GGA GTG GAT GTA 1200
 Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val
 385 390 395 400
 TCT ATC CCG TAC AGT TCT GAG AAC ACA TCC ATA TAC TGG CAG GAT GGA 1248
 Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly
 405 410 415
 GAC ATC CTG ACG ACG GCC ATC CTA CCT GAA GCT CTT GTC GTT AAG TTC 1296
 Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe
 420 425 430
 AAC TTT AAG CAG CTC CTT GTA GTT CAT ATC AGA GAT CCA TTC GAT GGA 1344
 Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly
 435 440 445
 AAG ACA TGC GGC ATA TGT GGT AAC TAT AAT CAA GAT TCA ACT GAT GAT 1392
 Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp
 450 455 460
 TTC TTT GAC GCA GAA GGA GCA TGC GCT CTG ACC CCC AAT CCC CCA GGA 1440
 Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly
 465 470 475 480
 TGT ACA GAG GAG CAG AAA CCA GAA GCT GAG CGA CTC TGC AAT AGT CTA 1488
 Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Ser Leu
 485 490 495
 TTT GAT AGT TCT ATC GAC GAG AAA TGT AAT GTC TGC TAC AAG CCT GAC 1536
 Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp
 500 505 510
 CGT ATT GCA CGA TGT ATG TAC GAG TAT TGC CTG AGG GGA CAG CAA GGA 1584
 Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly
 515 520 525
 TTC TGT GAC CAT GCT TGG GAG TTC AAA AAA GAA TGC TAC ATA AAG CAT 1632
 Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His
 530 535 540
 GGA GAC ACT CTA GAA GTA CCA CCT GAA TGC CAA TAA ATGAACAAAG 1677
 Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln
 545 550 555
 ATACAGAAGC TAAGACTACT ACAGCAGAAG ATAAAAGAGA AGCTGTAGTT CTTCAAAAAC 1737
 AGTATATTTT GATGTACTCA TTGTTTACTT ACATAAAAAT AAATTGTTAT TATCATAACG 1797
 TAAAGAAAAA AAAAAAAAAA AAAA

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(D) OTHER INFORMATION: *Luciola Cruciata* Luciferase (Firefly)

PATENT NO.: 4,968,613

ATG Met 1	GAA Glu	AAC Asn	ATG Met	GAA Glu 5	AAC Asn	GAT Asp	GAA Glu	AAT Asn	ATT Ile 10	GTA Val	GTT Val	GGA Gly	CCT Pro	AAA Lys 15	'CCG Pro	48
TTT Phe	TAC Tyr	CCT Pro	ATC Ile 20	GAA Glu	GAG Glu	GGA Gly	TCT Ser	GCT Ala 25	GGA Gly	ACA Thr	CAA Gln	TTA Leu	CGC Arg 30	AAA Lys	TAC Tyr	96
ATG Met	GAG Glu	CGA Arg 35	TAT Tyr	GCA Ala	AAA Lys	CTT Leu	GGC Gly 40	GCA Ala	ATT Ile	GCT Ala	TTT Phe	ACA Thr 45	AAT Asn	GCA Ala	GTT Val	144
ACT Thr	GGT Gly 50	GTT Val	GAT Asp	TAT Tyr	TCT Ser	TAC Tyr 55	GCC Ala	GAA Glu	TAC Tyr	TTG Leu	GAG Glu 60	AAA Lys	TCA Ser	TGT Cys	TGT Cys	192
CTA Leu 65	GGA Gly	AAA Lys	GCT Ala	TTG Leu 70	CAA Gln	AAT Asn	TAT Tyr	GGT Gly	TTG Leu	GTT Val 75	GTT Val	GAT Asp	GGC Gly	AGA Arg	ATT Ile 80	240
GCG Ala	TTA Leu	TGC Cys	AGT Ser	GAA Glu 85	AAC Asn	TGT Cys	GAA Glu	GAA Glu	TTT Phe 90	TTT Phe	ATT Ile	CCT Pro	GTA Val	ATA Ile 95	GCC Ala	288
GGA Gly	CTG Leu	TTT Phe	ATA Ile 100	GGT Gly	GTA Val	GGT Gly	GTT Val	GCA Ala 105	CCC Pro	ACT Thr	AAT Asn	GAG Glu	ATT Ile 110	TAC Tyr	ACT Thr	336
TTA Leu	CGT Arg	GAA Glu 115	CTG Leu	GTT Val	CAC His	AGT Ser	TTA Leu 120	GGT Gly	ATC Ile	TCT Ser	AAA Lys	CCA Pro 125	ACA Thr	ATT Ile	GTA Val	384
TTT Phe	AGT Ser 130	TCT Ser	AAA Lys	AAA Lys	GGC Gly	TTA Leu 135	GAT Asp	AAA Lys	GTT Val	ATA Ile	ACA Thr 140	GTA Val	CAG Gln	AAA Lys	ACA Thr	432
GTA Val 145	ACT Thr	ACT Thr	ATT Ile	AAA Lys	ACC Thr 150	ATT Ile	GTT Val	ATA Ile	CTA Leu	GAT Asp 155	AGC Ser	AAA Lys	GTT Val	GAT Asp	TAT Tyr 160	480
CGA Arg	GGA Gly	TAT Tyr	CAA Gln	TGT Cys 165	CTG Leu	GAC Asp	ACC Thr	TTT Phe	ATA Ile 170	AAA Lys	AGA Arg	AAC Asn	ACT Thr	CCA Pro 175	CCA Pro	528
GGT Gly	TTT Phe	CAA Gln 180	GCA Ala	TCC Ser	AGT Ser	TTC Phe	AAA Lys	ACT Thr 185	GTG Val	GAA Glu	GTT Val	GAC Asp	CGT Arg 190	AAA Lys	GAA Glu	576
CAA Gln	GTT Val	GCT Ala 195	CTT Leu	ATA Ile	ATG Met	AAC Asn	TCT Ser 200	TCG Ser	GGT Gly	TCT Ser	ACC Thr	GGT Gly 205	TTG Leu	CCA Pro	AAA Lys	624
GGC	GTA	CAA	CTT	ACT	CAC	GAA	AAT	ACA	GTC	ACT	AGA	TTT	TCT	CAT	GCT	672

465	470	475	480	
GAG CTT CCA GGA GCC GTT GTT GTA CTG GAA AGC GGA AAA AAT ATG ACC				1488
Glu Leu Pro Gly Ala Val Val Val Leu Glu Ser Gly Lys Asn Met Thr	485	490	495	
GAA AAA GAA GTA ATG GAT TAT GTT GCA AGT CAA GTT TCA AAT GCA AAA				1536
Glu Lys Glu Val Met Asp Tyr Val Als Ser Gln Val Ser Asn Ala Lys	500	505	510	
CGT TTA CGT GGT GGT GTT CGT TTT GTG GAT GAA GTA CCT AAA GGT CTT				1584
Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu	515	520	525	
ACT GGA AAA ATT GAC GGC AGA GCA ATT AGA GAA ATC CTT AAG AAA CCA				1632
Thr Gly Lys Ile Asp Gly Arg Ala Ile Arg Glu Ile Leu Lys Lys Pro	530	535	540	
GTT GCT AAG ATG				1644
Val Ala Lys Met				
545				

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1664
- (D) OTHER INFORMATION: Vargula (cypridina) luciferase

(x) PUBLICATION INFORMATION:

- JP 3-30678 Osaka (Tsuji)
- (A) Thompson *et al.*
- (C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
- (D) VOLUME: 86
- (F) PAGES: 1326-1332
- (G) DATE: (1989)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG AAG ATA ATA ATT CTG TCT GTT ATA TTG GCC TAC TGT GTC ACC GAC	48
Met Lys Ile Ile Ile Leu Ser Val Ile Leu Ala Tyr Cys Val Thr Asp	
1 5 10 15	
AAC TGT CAA GAT GCA TGT CCT GTA GAA GCG GAA CCG CCA TCA AGT ACA	96
Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Pro Pro Ser Ser Thr	
20 25 30	
CCA ACA GTT CCA ACT TCT TGT GAA GCT AAA GAA GGA GAA TGT ATA GAT	144
Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp	
35 40 45	
ACC AGA TGC GCA ACA TGT AAA CGA GAT ATA CTA TCA GAT GGA CTG TGT	192
Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys	
50 55 60	
GAA AAT AAA CCA GGG AAG ACA TGC TGT AGA ATG TGC CAG TAT GTG ATT	240
Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile	

65					70					75					80	
GAA	TGC	AGA	GTA	GAA	GCA	GCT	GGT	TAT	TTT	AGA	ACG	TTT	TAC	GGC	AAA	288
Glu	Cys	Arg	Val	Glu	Ala	Ala	Gly	Tyr	Phe	Arg	Thr	Phe	Tyr	Gly	Lys	
				85					90					95		
AGA	TTT	AAT	TTT	CAG	GAA	CCT	GGT	AAA	TAT	GTG	CTG	GCT	AGG	GGA	ACC	336
Arg	Phe	Asn	Phe	Gln	Glu	Pro	Gly	Lys	Tyr	Val	Leu	Ala	Arg	Gly	Thr	
			100					105					110			
AAG	GGT	GGC	GAT	TGG	TCT	GTA	ACC	CTC	ACC	ATG	GAG	AAT	CTA	GAT	GGA	384
Lys	Gly	Gly	Asp	Trp	Ser	Val	Thr	Leu	Thr	Met	Glu	Asn	Leu	Asp	Gly	
		115					120					125				
CAG	AAG	GGA	GCT	GTG	CTG	ACT	AAG	ACA	ACA	CTG	GAG	GTT	GCA	GGA	GAC	432
Gln	Lys	Gly	Ala	Val	Leu	Thr	Lys	Thr	Thr	Leu	Glu	Val	Ala	Gly	Asp	
	130					135					140					
GTA	ATA	GAC	ATT	ACT	CAA	GCT	ACT	GCA	GAT	CCT	ATC	ACA	GTT	AAC	GGA	480
Val	Ile	Asp	Ile	Thr	Gln	Ala	Thr	Ala	Asp	Pro	Ile	Thr	Val	Asn	Gly	
145					150					155					160	
GGA	GCT	GAC	CCA	GTT	ATC	GCT	AAC	CCG	TTC	ACA	ATT	GGT	GAG	GTG	ACC	528
Gly	Ala	Asp	Pro	Val	Ile	Ala	Asn	Pro	Phe	Thr	Ile	Gly	Glu	Val	Thr	
				165					170					175		
ATT	GCT	GTT	GTT	GAA	ATA	CCG	GGC	TTC	AAT	ATC	ACA	GTC	ATC	GAA	TTC	576
Ile	Ala	Val	Val	Glu	Ile	Pro	Gly	Phe	Asn	Ile	Thr	Val	Ile	Glu	Phe	
			180					185					190			
TTT	AAA	CTA	ATC	GTG	ATT	GAT	ATT	CTG	GGA	GGA	AGA	TCT	GTC	AGA	ATT	624
Phe	Lys	Leu	Ile	Val	Ile	Asp	Ile	Leu	Gly	Gly	Arg	Ser	Val	Arg	Ile	
		195					200					205				
GCT	CCA	GAC	ACA	GCA	AAC	AAA	GGA	CTG	ATA	TCT	GGT	ATC	TGT	GGT	AAT	672
Ala	Pro	Asp	Thr	Ala	Asn	Lys	Gly	Leu	Ile	Ser	Gly	Ile	Cys	Gly	Asn	
	210					215					220					
CTG	GAG	ATG	AAT	GAC	GCT	GAT	GAC	TTT	ACT	ACA	GAT	GCA	GAT	CAG	CTG	720
Leu	Glu	Met	Asn	Asp	Ala	Asp	Asp	Phe	Thr	Thr	Asp	Ala	Asp	Gln	Leu	
225					230					235				240		
GCG	ATC	CAA	CCC	AAC	ATA	AAC	AAA	GAG	TTC	GAC	GGC	TGC	CCA	TTC	TAT	768
Ala	Ile	Gln	Pro	Asn	Ile	Asn	Lys	Glu	Phe	Asp	Gly	Cys	Pro	Phe	Tyr	
				245					250					255		
GGC	AAT	CCT	TCT	GAT	ATC	GAA	TAC	TGC	AAA	GGT	CTG	ATG	GAG	CCA	TAC	816
Gly	Asn	Pro	Ser	Asp	Ile	Glu	Tyr	Cys	Lys	Gly	Leu	Met	Glu	Pro	Tyr	
			260					265					270			
AGA	GCT	GTA	TGT	CGT	AAC	AAT	ATC	AAC	TTC	TAC	TAT	TAC	ACT	CTA	TCC	864
Arg	Ala	Val	Cys	Arg	Asn	Asn	Ile	Asn	Phe	Tyr	Tyr	Tyr	Thr	Leu	Ser	
		275					280					285				
TGT	GCC	TTC	GCT	TAC	TGT	ATG	GGA	GGA	GAA	GAA	AGA	GCT	AAA	CAC	GTC	912
Cys	Ala	Phe	Ala	Tyr	Cys	Met	Gly	Gly	Glu	Glu	Arg	Ala	Lys	His	Val	
	290					295					300					
CTT	TTC	GAC	TAT	GTT	GAG	ACA	TGC	GCT	GCG	CCG	GAA	ACG	AGA	GGA	ACG	960
Leu	Phe	Asp	Tyr	Val	Glu	Thr	Cys	Ala	Ala	Pro	Glu	Thr	Arg	Gly	Thr	
305					310					315				320		
TGT	GTT	TTA	TCA	GGA	CAT	ACT	TTC	TAT	GAC	ACA	TTC	GAC	AAA	GCA	AGA	1008
Cys	Val	Leu	Ser	Gly	His	Thr	Phe	Tyr	Asp	Thr	Phe	Asp	Lys	Ala	Arg	
				325					330					335		

TAT CAA TTC CAG GGC CCA TGC AAG GAG ATT CTG ATG GCC GCA GAC TGT 1056
 Tyr Gln Phe Gln Gly Pro Cys Lys Glu Ile Leu Met Ala Ala Asp Cys
 340 345 350

TAC TGG AAC ACA TGG GAT GTA AAG GTT TCA CAT AGA GAC GTC GAA TCA 1104
 Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser
 355 360 365

TAC ACT GAG GTA GAG AAA GTA ACA ATC AGG AAA CAG TCA ACT GTA GTA 1152
 Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val
 370 375 380

GAT CTC ATT GTG GAT GGC AAG CAG GTC AAG GTT GGA GGA GTG GAT GTA 1200
 Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val
 385 390 395 400

TCT ATC CCG TAC AGC TCT GAG AAC ACT TCC ATA TAC TGG CAG GAT GGA 1248
 Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly
 405 410 415

GAC ATC CTG ACG ACG GCC ATC CTA CCT GAA GCT CTT GTC GTT AAG TTC 1296
 Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe
 420 425 430

AAC TTT AAG CAG CTC CTT GTA GTT CAT ATC AGA GAT CCA TTC GAT GCA 1344
 Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Ala
 435 440 445

AAG ACA TGC GGC ATA TGT GGT AAC TAT AAT CAA GAT TCA ACT GAT GAT 1392
 Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp
 450 455 460

TTC TTT GAC GCA GAA GGA GCA TGC GCT CTA ACC CCC AAC CCC CCA GGA 1440
 Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly
 465 470 475 480

TGT ACA GAG GAA CAG AAA CCA GAA GCT GAG CGA CTT TGC AAT AAT CTC 1488
 Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Asn Leu
 485 490 495

TTT GAT TCT TCT ATC GAC GAG AAA TGT AAT GTC TGC TAC AAG CCT GAC 1536
 Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp
 500 505 510

CGG ATT GCC CGA TGT ATG TAC GAG TAT TGC CTG AGG GGA CAA CAA GGA 1584
 Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly
 515 520 525

TTT TGT GAC CAT GCT TGG GAG TTC AAG AAA GAA TGC TAC ATA AAA CAT 1632
 Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His
 530 535 540

GGA GAC ACT CTA GAA GTA CCA CCT GAA TGT CAA TAA ACGTACAAAG 1677
 Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln
 545 550 555

ATACAGAAGC TAAGGCTACT ACAGCAGAAG ATAAAAAGA AACTGTAGTT CCTTCAAAAA 1737
 CCGTGTATTT TATGTACTCA TTGTTTAATT AGAGCAAAT AAATTGTTAT TATCATAACT 1797
 TAAACTAAAA AAAAAAAAAA AA 1819

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 115...702

(D) OTHER INFORMATION: apoaeguorin-encoding gene

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,093,240

(A) Inouye et al.

(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

(D) VOLUME: 82

(F) PAGES: 3154-3158

(G) DATE: (1985)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGAATGCAA TTCATCTTTG CATCAAAGAA      60
TTACATCAAA TCTCTAGTTG ATCAACTAAA TTGTCTCGAC AACAACAAGC AAAC ATG      117
                                     Met
                                     1
ACA AGC AAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC CCA      165
Thr Ser Lys Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn Pro
                    5                      10                      15
AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC AAC      213
Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val Asn
                20                      25                      30
CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT GAT      261
His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser Asp
                35                      40                      45
ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA CAC      309
Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg His
                50                      55                      60                      65
AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT GGT      357
Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly
                    70                      75                      80
GTG GAA ACT GAT TGG CCT GCA TAT ATT GAA GGA TGG AAA AAA TTG GCT      405
Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala
                    85                      90                      95
ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC CGT      453
Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg
                100                      105                      110
ATA TGG GGT GAT GCT TTG TTT GAT ATC GTT GAC AAA GAT CAA AAT GGA      501
Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn Gly

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115				120				125										
GCC	ATT	ACA	CTG	GAT	GAA	TGG	AAA	GCA	TAC	ACC	AAA	GCT	GCT	GGT	ATC	549		
Ala	Ile	Thr	Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ala	Ala	Gly	Ile			
130					135					140					145			
ATC	CAA	TCA	TCA	GAA	GAT	TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	ATT	597		
Ile	Gln	Ser	Ser	Glu	Asp	Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	Ile			
				150					155					160				
GAT	GAA	AGT	GGA	CAA	CTC	GAT	GTT	GAT	GAG	ATG	ACA	AGA	CAA	CAT	TTA	645		
Asp	Glu	Ser	Gly	Gln	Leu	Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His	Leu			
			165					170					175					
GGA	TTT	TGG	TAC	ACC	ATG	GAT	CCT	GCT	TGC	GAA	AAG	CTC	TAC	GGT	GGA	693		
Gly	Phe	Trp	Tyr	Thr	Met	Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly	Gly			
		180					185					190						
GCT	GTC	CCC	TAAGAAGCTC				TACGGTGGTG		ATGCACCCTA			GGAAGATGAT		GTGATTTTGA		752		
Ala	Val	Pro																
	195																	
ATAAAACACT			GATGAATTCA			ATCAAAATTT			TCCAAATTTT			TGAACGATTT			CAATCGTTTG			812
TGTTGATTTT			TGTAATTAGG			AACAGATTAA			ATCGAATGAT			TAGTTGTTTT			TTTAATCAAC			872
AGAACTTACA			AATCGAAAAA			GTAAAAAAA			AAAAAAAAAA			AAAAAAAAAA			AAAAAAAAAA			932
AAAAAAAAAA			AAAAAAAAAA			AAAAAA												958

ATG	ACC	AGC	GAA	CAA	TAC	TCA	GTC	AAG	CTT	ACA	CCA	GAC	TTC	GAC	AAC	48
Met	Thr	Ser	Glu	Gln	Tyr	Ser	Val	Lys	Leu	Thr	Pro	Asp	Phe	Asp	Asn	
1				5					10					15		
CCA	AAA	TGG	ATT	GGA	CGA	CAC	AAG	CAC	ATG	TTT	AAT	TTT	CTT	GAT	GTC	96
Pro	Lys	Trp	Ile	Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	
			20					25					30			

AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC 144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
35 40 45
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT 192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
50 55 60
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT 240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr
65 70 75 80
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG 288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
85 90 95
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT 336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
100 105 110
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT GAC AAA GAC CAA AAT 384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Asp Lys Asp Gln Asn
115 120 125
GGA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GAT GGC 432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Asp Gly
130 135 140
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT 480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145 150 155 160
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT 528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
165 170 175
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT 576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
180 185 190
GGA GCT GTC CCC TAA 591
Gly Ala Val Pro *
195

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Recombinant Aequorin AEQ2

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Prasher et al.
 (B) TITLE: Sequence Comparisons of Complementary
 DNAs Encoding Aequorin Isotypes
 (C) JOURNAL: Biochemistry
 (D) VOLUME: 26
 (F) PAGES: 1326-1332
 (G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn	
1 5 10 15	
CCA AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC	96
Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT	144
Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr	
65 70 75 80	
GGT GTG GAA ACT GAT TGG CCT GCA TAT ATT GAA GGA TGG AAA AAA TTG	288
Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu	
85 90 95	
GCT ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC	336
Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile	
100 105 110	
CGT ATA TGG GGT GAT GCT TTG TTC GAT ATC GTT GAC AAA GAT CAA AAT	384
Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn	
115 120 125	
GGA GCC ATT ACA CTG GAT GAA TGG AAA GCA TAC ACC AAA GCT GCT GGT	432
Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly	
130 135 140	
ATC ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	
ATT GAT GAA AGT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
GGA GCT GTC CCC TAA	591
Gly Ala Val Pro *	
195	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Recombinant Aequorin AEQ3

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Prasher et al.

(B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes

(C) JOURNAL: Biochemistry

(D) VOLUME: 26

(F) PAGES: 1326-1332

(G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG	ACC	AGC	GAA	CAA	TAC	TCA	GTC	AAG	CTT	ACA	TCA	GAC	TTC	GAC	AAC	48
Met	Thr	Ser	Glu	Gln	Tyr	Ser	Val	Lys	Leu	Thr	Ser	Asp	Phe	Asp	Asn	
1				5					10					15		
CCA	AGA	TGG	ATT	GGA	CGA	CAC	AAG	CAT	ATG	TTC	AAT	TTC	CTT	GAT	GTC	96
Pro	Arg	Trp	Ile	Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	
			20				25						30			
AAC	CAC	AAT	GGA	AAA	ATC	TCT	CTT	GAC	GAG	ATG	GTC	TAC	AAG	GCA	TCT	144
Asn	His	Asn	Gly	Lys	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	
		35					40					45				
GAT	ATT	GTC	ATC	AAT	AAC	CTT	GGA	GCA	ACA	CCT	GAG	CAA	GCC	AAA	CGA	192
Asp	Ile	Val	Ile	Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	
	50					55					60					
CAC	AAA	GAT	GCT	GTA	GGA	GAC	TTC	TTC	GGA	GGA	GCT	GGA	ATG	AAA	TAT	240
His	Lys	Asp	Ala	Val	Gly	Asp	Phe	Phe	Gly	Gly	Ala	Gly	Met	Lys	Tyr	
65					70				75					80		
GGT	GTG	GAA	ACT	GAT	TGG	CCT	GCA	TAC	ATT	GAA	GGA	TGG	AAA	AAA	TTG	288
Gly	Val	Glu	Thr	Asp	Trp	Pro	Ala	Tyr	Ile	Glu	Gly	Trp	Lys	Lys	Leu	
				85					90					95		
GCT	ACT	GAT	GAA	TTG	GAG	AAA	TAC	GCC	AAA	AAC	GAA	CCA	ACG	CTC	ATC	336
Ala	Thr	Asp	Glu	Leu	Glu	Lys	Tyr	Ala	Lys	Asn	Glu	Pro	Thr	Leu	Ile	
			100					105					110			
CGT	ATA	TGG	GGT	GAT	GCT	TTG	TTC	GAT	ATC	GTT	GAC	AAA	GAT	CAA	AAT	384
Arg	Ile	Trp	Gly	Asp	Ala	Leu	Phe	Asp	Ile	Val	Asp	Lys	Asp	Gln	Asn	
		115					120					125				
GGA	GCC	ATT	ACA	CTG	GAT	GAA	TGG	AAA	GCA	TAC	ACC	AAA	GCT	GCT	GGT	432
Gly	Ala	Ile	Thr	Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ala	Ala	Gly	

130	135	140	
ATC ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT			480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp			
145	150	155	160
ATT GAT GAA AAT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT			528
Ile Asp Glu Asn Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His			
165	170		175
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT			576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly			
180	185		190
GGA GCT GTC CCC TAA			591
Gly Ala Val Pro *			
195			

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...567

(D) OTHER INFORMATION: Aequorin photoprotein

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Charbonneau et al.

(B) TITLE: Amino acid sequence of the calcium-dependent photoprotein aequorin

(C) JOURNAL: Am. Chem. Soc.

(D) VOLUME: 24

(E) ISSUE: 24

(F) PAGES: 6762-6771

(G) DATE: 1985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTC AAG CTT ACA CCA GAC TTC GAC AAC CCA AAA TGG ATT GGA CGA CAC	48
Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His	
1	5
AAG CAC ATG TTT AAT TTT CTT GAT GTC AAC CAC AAT GGA AGG ATC TCT	96
Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser	
20	25
CTT GAC GAG ATG GTC TAC AAG GCG TCC GAT ATT GTT ATA AAC AAT CTT	144
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu	
35	40
GGA GCA ACA CCT GAA CAA GCC AAA CGT CAC AAA GAT GCT GTA GAA GCC	192
Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala	

50	55	60	
TTC TTC GGA GGA GCT GCA ATG AAA TAT GGT GTA GAA ACT GAA TGG CCT			240
Phe Phe Gly Gly Ala Ala Met Lys Tyr Gly Val Glu Thr Glu Trp Pro			
65	70	75	80
GAA TAC ATC GAA GGA TGG AAA AGA CTG GCT TCC GAG GAA TTG AAA AGG			288
Glu Tyr Ile Glu Gly Trp Lys Arg Leu Ala Ser Glu Glu Leu Lys Arg			
	85	90	95
TAT TCA AAA AAC CAA ATC ACA CTT ATT CGT TTA TGG GGT GAT GCA TTG			336
Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu			
	100	105	110
TTC GAT ATC ATT GAC AAA GAC CAA AAT GGA GCT ATT TCA CTG GAT GAA			384
Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Ser Leu Asp Glu			
	115	120	125
TGG AAA GCA TAC ACC AAA TCT GCT GGC ATC ATC CAA TCG TCA GAA GAT			432
Trp Lys Ala Tyr Thr Lys Ser Ala Gly Ile Ile Gln Ser Ser Glu Asp			
	130	135	140
TGC GAG GAA ACA TTC AGA GTG TGC GAT ATT GAT GAA AGT GGA CAG CTC			480
Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu			
	145	150	155
GAT GTT GAT GAG ATG ACA AGA CAA CAT TTA GGA TTT TGG TAC ACC ATG			528
Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met			
	165	170	175
GAT CCT GCT TGC GAA AAG CTC TAC GGT GGA GCT GTC CCC			567
Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro			
	180	185	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Aequorin mutant w/increased bioluminescence activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO: 10:

Asp 124 changed to Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn	

1	5	10	15	
CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC	96			
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val				
20 25 30				
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC	144			
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser				
35 40 45				
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT	192			
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg				
50 55 60				
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT	240			
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr				
65 70 75 80				
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG	288			
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu				
85 90 95				
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT	336			
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile				
100 105 110				
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT	384			
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn				
115 120 125				
GGA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GCT GGC	432			
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly				
130 135 140				
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480			
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp				
145 150 155 160				
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528			
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His				
165 170 175				
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576			
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly				
180 185 190				
GGA GCT GTC CCC	588			
Gly Ala Val Pro				
195				

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...588
 (D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant
 w/increased biolum. activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO:11:
 Glu 135 changed to Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn	
1 5 10 15	
CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC	96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC	144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr	
65 70 75 80	
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG	288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu	
85 90 95	
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT	336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile	
100 105 110	
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT	384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn	
115 120 125	
GGA GCT ATT TCA CTG GAT TCA TGG AAA GCA TAC ACC AAA TCT GCT GGC	432
Gly Ala Ile Ser Leu Asp Ser Trp Lys Ala Tyr Thr Lys Ser Ala Gly	
130 135 140	
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
GGA GCT GTC CCC	588
Gly Ala Val Pro	
195	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Recombinant site-directed
Aequorin mutant w/increased biolum. activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG	ACC	AGC	GAA	CAA	TAC	TCA	GTC	AAG	CTT	ACA	CCA	GAC	TTC	GAC	AAC	48
Met	Thr	Ser	Glu	Gln	Tyr	Ser	Val	Lys	Leu	Thr	Pro	Asp	Phe	Asp	Asn	
1				5					10					15		
CCA	AAA	TGG	ATT	GGA	CGA	CAC	AAG	CAC	ATG	TTT	AAT	TTT	CTT	GAT	GTC	96
Pro	Lys	Trp	Ile	Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	
			20					25					30			
AAC	CAC	AAT	GGA	AGG	ATC	TCT	CTT	GAC	GAG	ATG	GTC	TAC	AAG	GCG	TCC	144
Asn	His	Asn	Gly	Arg	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	
			35				40					45				
GAT	ATT	GTT	ATA	AAC	AAT	CTT	GGA	GCA	ACA	CCT	GAA	CAA	GCC	AAA	CGT	192
Asp	Ile	Val	Ile	Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	
	50					55					60					
CAC	AAA	GAT	GCT	GTA	GAA	GCC	TTC	TTC	GGA	GGA	GCT	GCA	ATG	AAA	TAT	240
His	Lys	Asp	Ala	Val	Glu	Ala	Phe	Phe	Gly	Gly	Ala	Ala	Met	Lys	Tyr	
65					70				75						80	
GGT	GTA	GAA	ACT	GAA	TGG	CCT	GAA	TAC	ATC	GAA	GGA	TGG	AAA	AGA	CTG	288
Gly	Val	Glu	Thr	Glu	Trp	Pro	Glu	Tyr	Ile	Glu	Gly	Trp	Lys	Arg	Leu	
				85					90					95		
GCT	TCC	GAG	GAA	TTG	AAA	AGG	TAT	TCA	AAA	AAC	CAA	ATC	ACA	CTT	ATT	336
Ala	Ser	Glu	Glu	Leu	Lys	Arg	Tyr	Ser	Lys	Asn	Gln	Ile	Thr	Leu	Ile	
			100					105					110			
CGT	TTA	TGG	GGT	GAT	GCA	TTG	TTC	GAT	ATC	ATT	TCC	AAA	GAC	CAA	AAT	384
Arg	Leu	Trp	Gly	Asp	Ala	Leu	Phe	Asp	Ile	Ile	Ser	Lys	Asp	Gln	Asn	
	115						120					125				
GCA	GCT	ATT	TCA	CTG	GAT	GAA	TGG	AAA	GCA	TAC	ACC	AAA	TCT	GCT	GGC	432
Ala	Ala	Ile	Ser	Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ser	Ala	Gly	
	130					135					140					
ATC	ATC	CAA	TCG	TCA	GAA	GAT	TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	480
Ile	Ile	Gln	Ser	Ser	Glu	Asp	Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	
145					150				155						160	

[illegible]

(2) INFORMATION FOR SEO ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- ```
(A) LENGTH: 567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
```

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...567  
(D) OTHER INFORMATION: Recombinant apoaequorin (AQUALITE®)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|                  |                   |                   |                   |                  |                  |                   |                   |                   |                  |                  |                   |                   |                   |                  |            |     |
|------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|------------|-----|
| AAG<br>Val<br>1  | CAC<br>Lys        | ATT<br>Leu        | ACA<br>Thr        | CCA<br>Pro<br>5  | GAC<br>Asp       | TTC<br>Phe        | GAC<br>Asp        | AAC<br>Asn        | CCA<br>Pro<br>10 | AAA<br>Lys       | TGG<br>Trp        | ATT<br>Ile        | GGA<br>Gly        | CGA<br>Arg<br>15 | CAC<br>His | 48  |
| AAG<br>Lys       | CAC<br>His        | ATG<br>Met<br>20  | TTT<br>Phe<br>20  | AAT<br>Asn       | TTT<br>Phe       | CTT<br>Leu        | GAT<br>Asp        | GTC<br>Val<br>25  | AAC<br>Asn       | CAC<br>His       | AAT<br>Asn        | GGA<br>Gly        | AGG<br>Arg<br>30  | ATC<br>Ile       | TCT<br>Ser | 96  |
| CTT<br>Leu       | GAC<br>Asp        | GAG<br>Glu<br>35  | ATG<br>Met        | GTC<br>Val       | TAC<br>Tyr       | AAG<br>Lys        | GCG<br>Ala<br>40  | TCC<br>Ser        | GAT<br>Asp       | ATT<br>Ile       | GTT<br>Val        | ATA<br>Ile<br>45  | AAC<br>Asn        | AAT<br>Asn       | CTT<br>Leu | 144 |
| GGA<br>Gly       | GCA<br>Ala<br>50  | ACA<br>Thr        | CCT<br>Pro        | GAA<br>Glu       | CAA<br>Gln<br>55 | GCC<br>Ala<br>55  | AAA<br>Lys        | CGT<br>Arg        | CAC<br>His       | AAA<br>Lys       | GAT<br>Asp<br>60  | GCT<br>Ala        | GTA<br>Val        | GAA<br>Glu       | GCC<br>Ala | 192 |
| TTC<br>Phe<br>65 | TTC<br>Phe        | GGA<br>Gly        | GGA<br>Gly        | GCT<br>Ala<br>70 | GGA<br>Gly<br>70 | ATG<br>Met        | AAA<br>Lys        | TAT<br>Tyr        | GGT<br>Gly       | GTA<br>Val<br>75 | GAA<br>Glu        | ACT<br>Thr        | GAA<br>Glu        | TGG<br>Trp<br>80 | CCT<br>Pro | 240 |
| GAA<br>Glu       | TAC<br>Tyr        | ATC<br>Ile        | GAA<br>Glu        | GGA<br>Gly<br>85 | TGG<br>Trp       | AAA<br>Lys        | AAA<br>Lys        | CTG<br>Leu        | GCT<br>Ala<br>90 | TCC<br>Ser       | GAG<br>Glu        | GAA<br>Glu        | TTG<br>Leu        | AAA<br>Lys<br>95 | AGG<br>Arg | 288 |
| TAT<br>Tyr       | TCA<br>Ser        | AAA<br>Lys        | AAC<br>Asn<br>100 | CAA<br>Gln       | ATC<br>Ile       | ACA<br>Thr        | CTT<br>Leu        | ATT<br>Ile<br>105 | CGT<br>Arg       | TTA<br>Leu       | TGG<br>Trp        | GGT<br>Gly        | GAT<br>Asp<br>110 | GCA<br>Ala       | TTG<br>Leu | 336 |
| TTC<br>Phe       | GAT<br>Asp        | ATC<br>Ile<br>115 | ATT<br>Ile        | GAC<br>Asp       | AAA<br>Lys       | GAC<br>Asp        | CAA<br>Gln<br>120 | AAT<br>Asn        | GGA<br>Gly       | GCT<br>Ala       | ATT<br>Ile        | CTG<br>Leu<br>125 | TCA<br>Ser        | GAT<br>Asp       | GAA<br>Glu | 384 |
| TGG<br>Trp       | AAA<br>Lys<br>130 | GCA<br>Ala        | TAC<br>Tyr        | ACC<br>Thr       | AAA<br>Lys       | TCT<br>Ser<br>135 | GAT<br>Asp        | GGC<br>Gly        | ATC<br>Ile       | ATC<br>Ile       | CAA<br>Gln<br>140 | TCG<br>Ser        | TCA<br>Ser        | GAA<br>Glu       | GAT<br>Asp | 432 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TGC | GAG | GAA | ACA | TTC | AGA | GTG | TGC | GAT | ATT | GAT | GAA | AGT | GGA | CAG | CTC | 480 |
| Cys | Glu | Glu | Thr | Phe | Arg | Val | Cys | Asp | Ile | Asp | Glu | Ser | Gly | Gln | Leu |     |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GAT | GTT | GAT | GAG | ATG | ACA | AGA | CAA | CAT | TTA | GGA | TTT | TGG | TAC | ACC | ATG | 528 |
| Asp | Val | Asp | Glu | Met | Thr | Arg | Gln | His | Leu | Gly | Phe | Trp | Tyr | Thr | Met |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GAT | CCT | GCT | TGC | GAA | AAG | CTC | TAC | GGT | GGA | GCT | GTC | CCC |     |     |     | 567 |
| Asp | Pro | Ala | Cys | Glu | Lys | Leu | Tyr | Gly | Gly | Ala | Val | Pro |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (x) PUBLICATION INFORMATION:

PATENT NO.: 5,484,723

## (ix) FEATURE:

(D) OTHER INFORMATION: Vibrio fisheri Flavin reductase

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Ile | Asn | Cys | Lys | Val | Lys | Ser | Ile | Glu | Pro | Leu | Ala | Cys | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Phe | Arg | Ile | Leu | Leu | His | Pro | Glu | Gln | Pro | Val | Ala | Phe | Lys | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Gln | Tyr | Leu | Thr | Val | Val | Met | Gly | Glu | Lys | Asp | Lys | Arg | Pro | Phe |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Ile | Ala | Ser | Ser | Pro | Cys | Arg | His | Glu | Gly | Glu | Ile | Glu | Leu | His |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Gly | Ala | Ala | Glu | His | Asn | Ala | Tyr | Ala | Gly | Glu | Val | Val | Glu | Ser |  |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Met | Lys | Ser | Ala | Leu | Glu | Thr | Gly | Gly | Asp | Ile | Leu | Ile | Asp | Ala | Pro |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| His | Gly | Glu | Ala | Trp | Ile | Arg | Glu | Asp | Ser | Asp | Arg | Ser | Met | Leu | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Ala | Gly | Gly | Thr | Gly | Phe | Ser | Tyr | Val | Arg | Ser | Ile | Leu | Asp | His |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Cys | Ile | Ser | Gln | Gln | Ile | Gln | Lys | Pro | Ile | Tyr | Leu | Tyr | Trp | Gly | Gly |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Arg | Asp | Glu | Cys | Gln | Leu | Tyr | Ala | Lys | Ala | Glu | Leu | Glu | Ser | Ile | Ala |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Gln | Ala | His | Ser | His | Ile | Thr | Phe | Val | Pro | Val | Val | Glu | Lys | Ser | Glu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Gly | Trp | Thr | Gly | Lys | Thr | Gly | Asn | Val | Leu | Glu | Ala | Val | Lys | Ala | Asp |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |  |  |
| Phe | Asn | Ser | Leu | Ala | Asp | Met | Asp | Ile | Tyr | Ile | Ala | Gly | Arg | Phe | Glu |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Met | Ala | Gly | Ala | Ala | Arg | Glu | Gln | Phe | Thr | Thr | Glu | Lys | Gln | Ala | Lys |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Lys | Glu | Gln | Leu | Phe | Gly | Asp | Ala | Phe | Ala | Phe | Ile |     |     |     |     |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |  |  |

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